

Raw Sequence Listing Error Summary

#6

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/470,168

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/470,168

DATE: 09/14/2000
TIME: 10:26:20

Input Set : A:\Gc538-2.APP.txt
Output Set: N:\CRF3\09142000\I470168.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Boston, Matthew Grant
4 Swanson, Barbara A.
6 <120> TITLE OF INVENTION: Method for Producing Ascorbic Acid Intermediates
8 <130> FILE REFERENCE: GC538
10 <140> CURRENT APPLICATION NUMBER: 09/470,168
11 <141> CURRENT FILING DATE: 1999-12-22
13 <150> PRIOR APPLICATION NUMBER: 09/218,700
14 <151> PRIOR FILING DATE: 1998-12-22
16 <160> NUMBER OF SEQ ID NOS: 2
18 <170> SOFTWARE: FastSEQ for Windows Version 3.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 31
22 <212> TYPE: DNA
23 <213> ORGANISM: Synthetic
25 <400> SEQUENCE: 1
26 agggagtgtct tactacctta tctgcggtat a
28 <210> SEQ ID NO: 2
29 <211> LENGTH: 31
30 <212> TYPE: DNA
31 <213> ORGANISM: Synthetic
33 <400> SEQUENCE: 2
34 cgctagtgtg gcaatccatt gattttgcac a

*invalid response - per new sequence rules, the only
valid responses are:
Unknown,
Artificial Sequence,
or scientific name
(genus/species)*

*see circled portion
of item 12 on Enov
Summary Sheet*

VERIFICATION SUMMARY

DATE: 09/14/2000

PATENT APPLICATION: US/09/470,168

TIME: 10:26:21

Input Set : A:\Gc538-2.APP.txt

Output Set: N:\CRF3\09142000\I470168.raw